

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/870,762ADATE: 08/31/98
TIME: 16:56:52

INPUT SET: S28314.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT: Duft, Bradford
6 Kolterman, Orville
7
8 (ii) TITLE OF THE INVENTION: METHODS FOR TREATING OBESITY
9
10 (iii) NUMBER OF SEQUENCES: 15
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: LYON & LYON
14 (B) STREET: 633 WEST FIFTH STREET, SUITE 4700
15 (C) CITY: LOS ANGELES
16 (D) STATE: CA
17 (E) COUNTRY: USA
18 (F) ZIP: 90071-2066
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Diskette
22 (B) COMPUTER: IBM Compatible
23 (C) OPERATING SYSTEM: DOS
24 (D) SOFTWARE: FastSEQ Version 2.0
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: 08/870,762
28 (B) FILING DATE: 06-JUN-1997
29 (C) CLASSIFICATION:
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER:
33 (B) FILING DATE:
34
35
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: DUFT, BRADFORD J
38 (B) REGISTRATION NUMBER: 32,219
39 (C) REFERENCE/DOCKET NUMBER: 226/104
40
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: 619-552-2200
43 (B) TELEFAX: 619-552-0159
44 (C) TELEX:
45
46

RAW SEQUENCE LISTING

PATENT APPLICATION US/08/870,762A

DATE: 08/31/98
TIME: 16:56:53

INPUT SET: S28314.raw

47 (2) INFORMATION FOR SEQ ID NO:1:

48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 37 amino acids

51 (B) TYPE: amino acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

54

55 (ii) MOLECULE TYPE: peptide

56

57 (ix) FEATURE:

58 (B) LOCATION: 2,7

59 (D) OTHER INFORMATION: disulfide bridge between
60 the Cys residues

61 (B) LOCATION: 37

62 (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

63

64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

65

66

67 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

68 1 5 10 15

69 Leu Val His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr

70 20 25 30

71 Asn Val Gly Ser Asn Thr Tyr

72 35

73

74 (2) INFORMATION FOR SEQ ID NO:2:

75

76 (i) SEQUENCE CHARACTERISTICS:

77 (A) LENGTH: 37 amino acids

78 (B) TYPE: amino acid

79 (C) STRANDEDNESS: single

80 (D) TOPOLOGY: linear

81

82 (ii) MOLECULE TYPE: peptide

83

84 (ix) FEATURE:

85 (B) LOCATION: 2,7

86 (D) OTHER INFORMATION: disulfide bridge between
87 the Cys residues

88 (B) LOCATION: 37

89 (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

90

91

92

93

94 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

95

96 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

97 1 5 10 15

98 Leu Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr

99 20 25 30

RAW SEQUENCE LISTING PATENT APPLICATION US/08/870,762A

DATE: 08/31/98
TIME: 16:56:54

INPUT SET: S28314.raw

100 Asn Val Gly Ser Asn Thr Tyr

101 35

102

103

104

105 (2) INFORMATION FOR SEQ ID NO:3:

106

107 (i) SEQUENCE CHARACTERISTICS:

108 (A) LENGTH: 37 amino acids

109 (B) TYPE: amino acid

110 (C) STRANDEDNESS: single

111 (D) TOPOLOGY: linear

112

113 (ii) MOLECULE TYPE: Peptide

114

115 (ix) FEATURE:

116 (B) LOCATION: 2,7

117 (D) OTHER INFORMATION: disulfide bridge between
118 the Cys residues

119 (B) LOCATION: 37

120 (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

121

122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

123

124 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

125 1 5 10 15

126 Leu Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr

127 20 25 30

128 Asn Val Gly Ser Asn Thr Tyr

129 35

130

131 (2) INFORMATION FOR SEQ ID NO:4:

132

133 (i) SEQUENCE CHARACTERISTICS:

134 (A) LENGTH: 37 amino acids

135 (B) TYPE: amino acid

136 (C) STRANDEDNESS: single

137 (D) TOPOLOGY: linear

138

139 (ii) MOLECULE TYPE: Peptide

140

141 (ix) FEATURE:

142 (B) LOCATION: 2,7

143 (D) OTHER INFORMATION: disulfide bridge between
144 the Cys residues

145 (B) LOCATION: 37

146 (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)

147

148 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

149

150 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

151 1 5 10 15

152 Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Pro Ser Thr

INPUT SET: S28314.raw

```

153              20              25              30
154 Asn Val Gly Ser Asn Thr Tyr
155              35
156
157          (2) INFORMATION FOR SEQ ID NO:5:
158
159      (i) SEQUENCE CHARACTERISTICS:
160          (A) LENGTH: 37 amino acids
161          (B) TYPE: amino acid
162          (C) STRANDEDNESS: single
163          (D) TOPOLOGY: linear
164
165      (ii) MOLECULE TYPE: peptide
166
167      (ix) FEATURE:
168          (B) LOCATION: 2,7
169          (D) OTHER INFORMATION: disulfide bridge between
170                                the Cys residues
171          (B) LOCATION: 37
172          (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
173
174      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
175
176 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
177   1              5              10              15
178 Leu Val His Ser Ser Asn Asn Phe Gly Pro Val Leu Pro Pro Thr
179              20              25              30
180 Asn Val Gly Ser Asn Thr Tyr
181              35
182
183
184          (2) INFORMATION FOR SEQ ID NO:6:
185
186      (i) SEQUENCE CHARACTERISTICS:
187          (A) LENGTH: 37 amino acids
188          (B) TYPE: amino acid
189          (C) STRANDEDNESS: single
190          (D) TOPOLOGY: linear
191
192      (ii) MOLECULE TYPE: peptide
193
194      (ix) FEATURE:
195          (B) LOCATION: 2,7
196          (D) OTHER INFORMATION: linkage between the Asp and
197                                Lys residues
198          (B) LOCATION: 37
199          (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
200
201      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
202
203 Lys Asp Asn Thr Ala Thr Lys Ala Thr Gln Arg Leu Ala Asn Phe
204   1              5              10              15
205 Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr

```

INPUT SET: S28314.raw

206 20 25 30
207 Asn Val Gly Ser Asn Thr Tyr
208 35
209
210
211 (2) INFORMATION FOR SEQ ID NO:7:
212
213 (i) SEQUENCE CHARACTERISTICS:
214 (A) LENGTH: 36 amino acids
215 (B) TYPE: amino acid
216 (C) STRANDEDNESS: single
217 (D) TOPOLOGY: linear
218
219 (ii) MOLECULE TYPE: peptide
220
221 (ix) FEATURE:
222 (B) LOCATION: 1,6
223 (D) OTHER INFORMATION: disulfide bridge between
224 the Cys residues
225 (B) LOCATION: 36
226 (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
227
228 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
229
230 Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
231 1 5 10 15
232 Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr Asn
233 20 25 30
234 Val Gly Ser Asn Thr Tyr
235 35
236
237
238
239 (2) INFORMATION FOR SEQ ID NO:8:
240
241 (i) SEQUENCE CHARACTERISTICS:
242 (A) LENGTH: 37 amino acids
243 (B) TYPE: amino acid
244 (C) STRANDEDNESS: single
245 (D) TOPOLOGY: linear
246
247 (ii) MOLECULE TYPE: peptide
248
249 (ix) FEATURE:
250 (B) LOCATION: 2,7
251 (D) OTHER INFORMATION: disulfide bridge between
252 the Cys residues
253 (B) LOCATION: 37
254 (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
255
256 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
257
258

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/870,762A

DATE: 08/31/98
TIME: 16:56:56

INPUT SET: S28314.raw

Line

Error

Original Text